

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ceriani, Roberto L.
Peterson, Jerry A.
Larocca, David J.

(ii) TITLE OF THE INVENTION: FUSION PROTEIN WITH 46 KDALTON
HMFG DIFFERENTIATION ANTIGEN
BINDING SPECIFICITY, COMPOSITION,
KIT & METHODS

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Pennsylvania
(D) STATE: USA
(E) COUNTRY: 19482
(F) ZIP:

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk 3.5"
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
(D) SOFTWARE: PatentIn #1.0,
Version #1.25

B2
(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: January 2, 2002
(C) CLASSIFICATION:

PARENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/482,596
(B) FILING DATE: June 7, 1995
(C) CLASSIFICATION:

grand parent APPLICATION DATA:
(A) APPLICATION NUMBER: 07/607,538
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Amzel, Viviana
(B) REGISTRATION No.: 30,930
(C) REFERENCE/DOCKET No: CRFC-047

(ix) TELECOMMUNICATION INFORMATION:
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(C) TELEX: N.A.

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1384 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATTCATCC ATGATGTTAA TAAAAAACAC AAGGAGTTG TGGGTAACTG 50
GAACAAAAAC GCGGTGCATG TCAACCTGTT TGAGACCCCT GTGGAGGCTC 100
AGTACGTGAG ATTGTACCCC ACGAGCTGCC ACACGGCCTG CACTCTGC 150
TTTGAGCTAC TGGGCTGTGA GCTGAACGGA TGCGCCAATC CCCTGGGC 200
GAAGAATAAC AGCATCCCTG ACAAGCAGAT CACGGCCTCC AGCAGCTACA 250
AGACCTGGGG CTTGCATCTC TTCAGCTGGA ACCCCTCCTA TGACGGCTG 300
GACAAGCAGG GCAACTCAA CGCCTGGGTT GCGGGGAGCT ACGGTAACGA 350
TCAGTGGCTG CAGGTGGACC TGGGCTCCTC GAAGGAGGTG ACAGGCATCA 400
TCACCCAGGG GGCCCGTAAC TTGGCTCTG TCCAGTTTGT GGCATCCTAC 450
AAGGTTGCCT ACAGTAATGA CAGTGCAGAC TGGACTGAGT ACCAGGACCC 500
CAGGACTGGC AGCAGTAAGA TCTTCCCTGG CAACTGGAC AACCACTCCC 550
ACAAGAAGAA CTTGTTGAG ACGCCCATCC TGGCTCGCTA TGTGCGCATC 600
CTGCCCTGAG CCTGGCACAA CGGCATCGCC CTGCGCCTGG AGCTGCTGGG 650
CTGTTAGTGG CCACCTGCCA CCCCCCAGGTC TTCCCTGCTTT CCATGGGCC 700
GCTGCCTCTT GGCTTCTCAG CCCCTTTAAA TCACCATAGG GCTGGGGACT 750
GGGGAAGGGG AGGGTGTCA GAGGCAGCAC CACCACACAG TCACCCCTCC 800
CTCCCTCTT CCCACCTCTC ACCTCTCAGC GGCCCTGCC CAGCCCTAA 850
GCCCGTCCC CTAACCCCCA GTCCCTACTG TCCTGTTTC TTAGGCACTG 900
AGGGATCTGA GTAGGTCTGG GATGGACAGG AAAGGGAAA GTAGGGCGTG 950
TGGTTTCCCT GCCCCCTGTCC GGACCGCCGA TCCCAGGTGC GTGTGTCTCT 1000
GTCTCTCTTA GCCCCCTCTC CACACATCAC ATTCCCATGG TGGCCTCAAG 1050
AAAGGCCGG AAGCCCCAGG CTGGAGATAA CAGCCTCTTG CCCGTCGGCC 1100
CTGCGTCGGC CCTGGGGTAC CATGTGCCAC AACTGCTGTG GCCCCCTGTC 1150
CCCAAGACAC TTCCCTCTGT CTCCCTGGTT GCCTCTCTTG CCCCTTGTC 1200
TGAAGCCCAG CGACACAGAA GGGGGTGGGG CGGGTCTATG GGGAGAAAGG 1250
GAGCGAGGTC AGAGGAGGGC ATGGGTTGGC AGGGTGGGCG TTTGGGGCCC 1300
TCATGCTGGC TTTTCACCCC AGAGGACACA GGCAGCTTCC AAAATATATT 1350
TATCTTCTTC ACGGGAAAAA AAAAAAAAAA ACCG 1384

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val
1 5 10
Gly Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu
15 20 25
Thr Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser
30 35 40
Cys His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys
45 50 55
Glu Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn
60 65 70
Ser Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys
75 80
Thr Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala
85 90 95
Arg Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly
100 105 110
Ser Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser
115 120 125
Ser Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn
130 135 140
Phe Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr
145 150
Ser Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg
155 160 165
Thr Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His
170 175 180
Ser His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg
185 190 195
Tyr Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala
200 205 210
Leu Arg Leu Glu Leu Leu Gly Cys
215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 217
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Ile His Asp Val Asn Lys Lys His Lys Glu Phe Val Gly
1 5 10
Asn Trp Asn Lys Asn Ala Val His Val Asn Leu Phe Glu Thr
15 20 25
Pro Val Glu Ala Gln Tyr Val Arg Leu Tyr Pro Thr Ser Cys
30 35 40
His Thr Ala Cys Thr Leu Arg Phe Glu Leu Leu Gly Cys Glu
45 50 55
Leu Asn Gly Cys Ala Asn Pro Leu Gly Leu Lys Asn Asn Ser
60 65 70
Ile Pro Asp Lys Gln Ile Thr Ala Ser Ser Ser Tyr Lys Thr
75 80
Trp Gly Leu His Leu Phe Ser Trp Asn Pro Ser Tyr Ala Arg
85 90 95
Leu Asp Lys Gln Gly Asn Phe Asn Ala Trp Val Ala Gly Ser

100 105 110
Tyr Gly Asn Asp Gln Trp Leu Gln Val Asp Leu Gly Ser Ser
115 120 120
Lys Glu Val Thr Gly Ile Ile Thr Gln Gly Ala Arg Asn Phe
130 135 140
Gly Ser Val Gln Phe Val Ala Ser Tyr Lys Val Ala Tyr Ser
145 150
Asn Asp Ser Ala Asn Trp Thr Glu Tyr Gln Asp Pro Arg Thr
155 160 165
Gly Ser Ser Lys Ile Phe Pro Gly Asn Trp Asp Asn His Ser
170 175 180
His Lys Lys Asn Leu Phe Glu Thr Pro Ile Leu Ala Arg Tyr
185 190 195
Val Arg Ile Leu Pro Val Ala Trp His Asn Arg Ile Ala Leu
200 205 210
Arg Leu Glu Leu Leu Gly Cys
215 217

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

B7N
Phe Lys Gly Asn Ser Thr Arg Asn Val Met Tyr Phe Asn Gly
1 5 10
Asn Ser Asp Ala Ser Thr Ile Lys Glu Asn Gln Phe Asp Pro
15 20 25
Pro Ile Val Ala Arg Tyr Ile Arg Ile Ser Pro Thr Arg Ala
30 35 40
Tyr Asn Arg Pro Thr Leu Arg Leu Glu Leu Gln Gly Cys Glu
45 50 55
Val Asn Gly Cys Ser Thr Pro Leu Gly Met Glu Asn Gly Lys
60 65 70
Ile Glu Asn Lys Gln Ile Thr Ala Ser Ser Phe Lys Lys Ser
75 80
Trp Trp Gly Asp Tyr Trp Glu Pro Phe Arg Ala Arg Leu Asn
85 90 95
Ala Gln Gly Arg Val Asn Ala Trp Gln Ala Lys Ala Asn Asn
100 105 110
Asn Lys Gln Trp Leu Glu Ile Asp Leu Leu Lys Ile Lys Lys
115 120 125
Ile Thr Ala Ile Ile Thr Gln Gly Cys Lys Ser Leu Ser Ser
130 135 140
Glu Met Tyr Val Lys Ser Tyr Thr Ile His Tyr Ser Glu Gln
145 150
Gly Val Glu Trp Lys Pro Tyr Arg Leu Lys Ser Ser Met Val
155 160 165
Asp Lys Ile Phe Glu Gly Asn Thr Asn Thr Lys Gly His Val
170 175 180
Lys Asn Phe Phe Asn Pro Pro Ile Ile Ser Arg Phe Ile Arg
185 190 195
Val Ile Pro Lys Thr Trp Asn Gln Ser Ile Ala Leu Arg Leu
200 205 210

Glu Leu Phe Gly Cys Asp Ile Tyr
215 218

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 218
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly
1 5 10
Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro
15 20 25
Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr
30 35 40
Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp
45 50 55
Leu Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala
60 65 70
Ile Ser Asp Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn
75 80
Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu His Leu
85 90 95
Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro
100 105 110
Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val
115 120 125
Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr Glu
130 135 140
Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly
145 150
His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val
155 160 165
Phe Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser
170 175 180
Leu Asp Pro Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro
185 190 195
Gln Ser Trp Val Val His Gln Ile Ala Leu Arg Met Glu Val Leu
200 205 210
Gly Cys Glu Ala Gln Asp Leu Tyr

215 218